E. Y. Elwan
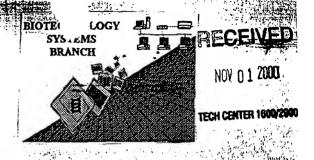
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/117, 921 A_

Source: _1638_

Date Processed by STIC: _10-25-00_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

1638

```
RAW SEQUENCE LISTING              DATE: 10/25/2000
PATENT APPLICATION:  US/09/117,921A    TIME: 17:32:14

     Input Set : A:\BROUN1.APP.txt
     Output Set: N:\CRF3\10252000\I117921A.raw

  3 <110> APPLICANT: BROUN, Pierre
  4        VAN DE LOO, Frank
  5        BODDUPALLI, Sekhar
  6        SOMERVILLE, Chris
  8 <120> TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY
  9        MODIFIED PLANTS
 11 <130> FILE REFERENCE: 20263/255164
 13 <140> CURRENT APPLICATION NUMBER: 09/117,921A
 14 <141> CURRENT FILING DATE: 1999-03-04
 16 <150> PRIOR APPLICATION NUMBER: 08/597,313
 17 <151> PRIOR FILING DATE: 1996-02-06
 19 <150> PRIOR APPLICATION NUMBER: PCT/US97/02187
 20 <151> PRIOR FILING DATE: 1997-02-06
 22 <160> NUMBER OF SEQ ID NOS: 15
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 543
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Lesquerella fendleri
 31 <220> FEATURE:
 32 <221> NAME/KEY: primer_bind
 33 <222> LOCATION: (83)
 34 <223> OTHER INFORMATION: nucleotide sequence of pLesq2
 36 <400> SEQUENCE: 1
 37 tattggcacc ggcggcacca ttccaacaat ggatccctag aaaaagatga agtctttgtc 60
 38 ccacctaaga aagctgcagt camatggtat gtcaaatacc tcaacaaccc tcttggacgc 120
 39 attctggtgt taacagttca gtttatcctc gggtggcctt tgtatctagc ctttaatgta 180
 40 tcaggtagac cttatgatgg tttcgcttca catttcttcc ctcatgcacc tatctttaag 240
 41 gaccgtgaac gtctccagat atacatctca gatgctggta ttctagctgt ctgttatggt 300
 42 ctttaccgtt acgctgcttc acaaggattg actgctatga tctgcgtcta cggagtaccg 360
 43 cttttgatag tgaacttttt ccttgtcttg gtcacttct tgcagcacac tcatccttca 420
 44 ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggt tacggtagac 480
 45 agagactatg gaatcttgaa caaggtgttt cacaacataa cagacaccca cgtagcacac 540
 46 cac                                                      543
 49 <210> SEQ ID NO: 2
 50 <211> LENGTH: 544
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Lesquerella fendleri
 54 <400> SEQUENCE: 2
 55 tataggcacc ggaggcacca ttccaacaca ggatccctcg aaagagatga agtatttgtc 60
 56 ccaaagcaga aatccgcaat caagtggtac ggcgaatacc tcaacaaccc tcctggtcgc 120
 57 atcatgatgt taactgtcca gttcgtcctc ggatggccct tgtacttagc cttcaacgtt 180
 58 tctggcagac cctacaatgg tttcgcttcc catttcttcc ccaatgctcc tatctacaac 240
 59 gaccgtgaac gcctccagat ttacatctct gatgctggta ttctagccgt ctgttatggt 300
 60 ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagttccg 360
 61 cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcaccctgcg 420
 62 ttgcctcact atgattcatc agagtgggat tggcttagag gagctttagc tactgtagac 480
```

W--> 38 (handwritten arrow pointing to line 38; "a" circled in "camatggtat")

→ What does "n" represent?
"n" may only represent a single base.
see #10 on the Error Summary Sheet

RAW SEQUENCE LISTING   DATE: 10/25/2000
PATENT APPLICATION: US/09/117,921A   TIME: 17:32:14

Input Set : A:\BROUN1.APP.txt
Output Set: N:\CRF3\10252000\I117921A.raw

```
     63 agagactatg gaatcttgaa caaggtgttc cataacatca cagacaccca cgtcgcacac 540
     64 cact                                                              544
     67 <210> SEQ ID NO: 3
     68 <211> LENGTH: 1855
     69 <212> TYPE: DNA
     70 <213> ORGANISM: Lesquerella fendleri
     72 <220> FEATURE:
     73 <221> NAME/KEY: gene
     74 <222> LOCATION: (1)..(1855)
     75 <223> OTHER INFORMATION: genomic clone encoding pLesq-HYD
     77 <400> SEQUENCE: 3
W--> 78 atgaagcttt ataagaagtt agttttctct ggtgacagag aaatcntgtc aattggtagt 60
W--> 79 gacagttgaa gcaacaggaa caacaaggat ggttggtcnt gatgctgatg tggtgatgtg 120
     80 ttattcatca aatactaaat actacattac ttgttgctgc ctacttctcc tatttcctcc 180
W--> 81 gccacccatt ttggacccac gcncttcca tttaaaccct ctctcgtgct attcaccaga 240
     82 agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcatcgtta 300
     83 ttaacgtaag ttttttttga ccactcatat ctaaaatcta gtacatgcaa tagattaatg 360
     84 actgttcctt cttttgatat tttcagcttc ttgaattcaa gatgggtgct ggtggaagaa 420
     85 taatggttac ccctctcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480
     86 agaaaccacc attcactgtt aaagatctga agaaagcaat cccacagcat tgtttcaagc 540
     87 gctctatccc tcgttctttc tcctacctc tcacagatat cactttagtt tcttgcttct 600
     88 actacgttgc cacaaattac ttctctcttc ttcctcagcc tctctctact tacctagctt 660
     89 ggcctctcta ttgggtatgt caaggctgtg tcttaaccgg tatctgggtc attggccatg 720
     90 aatgtggtca ccatgcattc agtgactatc aatgggtaga tgcactgtt ggttttatct 780
     91 tccattcctt ccttctcgtc ccttacttct cctggaaata cagtcatcgt cgtcaccatt 840
     92 ccaacaatgg atctctcgag aaagatgaag tctttgtccc accgaagaaa gctgcagtca 900
     93 aatggtatgt taaatacctc aacaaccctc ttggacgcat tctggtgtta acagttcagt 960
     94 ttatcctcgg gtggcctttg tatctagcct ttaatgtatc aggtagacct tatgatggtt 1020
     95 tcgcttcaca tttcttccct catgcaccta tctttaaaga ccgagaacgc ctccagatat 1080
     96 acatctcaga tgctggtatt ctagctgtct gttatggtct ttaccgttac gctgcttcac 1140
     97 aaggattgac tgctatgatc tgcgtctatg gagtaccgct tttgatagtg aacttttttcc 1200
     98 ttgtcttggt aactttcttg cagcacactc atccttcgtt acctcattat gattcaaccg 1260
     99 agtgggaatg gattagagga gctttggtta cggtagacag agactatgga atattgaaca 1320
    100 aggtgttcca taacataaca gacacacatg tggctcatca tctctttgca actataccgc 1380
    101 attataacgc aatggaagct acagaggcga taaagccaat acttggtgat tactaccact 1440
    102 tcgatggaac accgtggtat gtggccatgt atagggaagc aaaggagtgt ctctatgtag 1500
    103 aaccggatac ggaacgtggg aagaaaggtg tctactatta caacaataag ttatgaggct 1560
    104 gatagggcga gagaagtgca attatcaatc ttcatttcca tgttttaggt gtcttgttta 1620
W--> 105 agaagctatg ctttgtttca ataatctcag agtccatnca gttgtgttct ggtgcatttt 1680
    106 gcctagttat gtggtgtcgg aagttagtgt tcaaactgct tcctgctgtg ctgcccagtg 1740
W--> 107 aagaacaagt ttacgtgttt aaaatactcg gaacgaattg accacanat atccaaaacc 1800
    108 ggctatccga attccatatc cgaaaaccgg atatccaaat ttccagagta cttag       1855
    111 <210> SEQ ID NO: 4
    112 <211> LENGTH: 384
    113 <212> TYPE: PRT
    114 <213> ORGANISM: Lesquerella fendleri
    116 <400> SEQUENCE: 4
    117 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
    118   1               5                  10                  15
```

Missing mandatory feature <220> to <223> to explain "n's" in the sequence. See #10 on the Error Summary Sheet.

Input Set : A:\BROUN1.APP.txt
Output Set: N:\CRF3\10252000\I117921A.raw

```
120 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
121              20                  25                  30
123 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
124          35                  40         .          45
126 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
127          50                  55                  60
129 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
130  65                  70                  75                  80
132 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
133                  85                  90                  95
135 Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
136              100                 105                 110
138 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
139          115                 120                 125
141 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
142          130                 135                 140
144 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
145 145                 150                 155                 160
147 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
148              165                 170                 175
150 Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
151              180                 185                 190
153 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
154          195                 200                 205
156 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
157          210                 215                 220
159 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
160 225                 230                 235                 240
162 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
163                  245                 250                 255
165 Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
166              260                 265                 270
168 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
169          275                 280                 285
171 Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
172          290                 295                 300
174 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
175 305                 310                 315                 320
177 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
178                  325                 330                 335
180 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
181          340                 345                 350
183 Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
184          355         .       360                 365
186 Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
187          370                 375                 380
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 387
195 <212> TYPE: PRT
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/117,921A

DATE: 10/25/2000
TIME: 17:32:14

Input Set : A:\BROUN1.APP.txt
Output Set: N:\CRF3\10252000\I117921A.raw

```
196 <213> ORGANISM: Ricinus communis
198 <400> SEQUENCE: 5
199 Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
200  1               5                  10                  15
202 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
203              20                  25                  30
205 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
206          35                  40                  45
208 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
209      50                  55                  60
211 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
212  65              70                  75                  80
214 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
215              85                  90                  95
217 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
218             100                 105                 110
220 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
221         115                 120                 125
223 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
224         130                 135                 140
226 His Arg Arg His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
227 145                 150                 155                 160
229 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
230             165                 170                 175
232 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
233             180                 185                 190
235 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
236         195                 200                 205
238 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
239         210                 215                 220
241 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
242 225                 230                 235                 240
244 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
245             245                 250                 255
247 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
248             260                 265                 270
250 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
251         275                 280                 285
253 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
254         290                 295                 300
256 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
257 305                 310                 315                 320
259 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
260             325                 330                 335
262 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
263             340                 345                 350
265 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
266         355                 360                 365
268 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
```

```
269      370                  375                  380
271 Asn Lys Tyr
272 385
275 <210> SEQ ID NO: 6
276 <211> LENGTH: 383
277 <212> TYPE: PRT
278 <213> ORGANISM: Arabidopsis thaliana
280 <400> SEQUENCE: 6
281 Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
282  1               5                  10                  15
284 Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
285              20                  25                  30
287 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
288          35                  40                  45
290 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
291      50                  55                  60
293 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
294  65                  70                  75                  80
296 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
297              85                  90                  95
299 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
300             100                 105                 110
302 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
303             115                 120                 125
305 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
306          130                 135                 140
308 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
309 145                 150                 155                 160
311 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
312              165                 170                 175
314 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
315             180                 185                 190
317 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
318          195                 200                 205
320 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
321          210                 215                 220
323 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
324 225                 230                 235                 240
326 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
327              245                 250                 255
329 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
330             260                 265                 270
332 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
333          275                 280                 285
335 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
336          290                 295                 300
338 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
339 305                 310                 315                 320
341 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
```

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 10/25/2000
PATENT APPLICATION: US/09/117,921A   TIME: 17:32:15

Input Set : A:\BROUN1.APP.txt
Output Set: N:\CRF3\10252000\I117921A.raw

```
L:38  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:78  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:79  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:81  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
```